04C0
#4

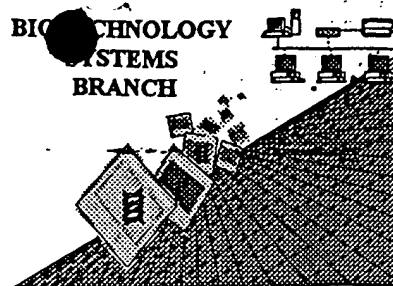# RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY SYSTEMS BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/645,593_

Source: _OIPE_

Date Processed by STIC: _9/7/2000_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: *09/445,593* |

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

RAW SEQUENCE LISTING   DATE: 09/07/2000
PATENT APPLICATION: US/09/645,593   TIME: 14:27:09

Input Set : A:\Sequence
Output Set: N:\CRF3\09072000\I645593.raw

```
 4 <110> APPLICANT: Chaudhary, Sarita
 5         van Rooijen, Gijs
 6         Moloney, Maurice
 7         Singh, Surinder
 9 <120> TITLE OF INVENTION: Flax Seed Specific Promoters
11 <130> FILE REFERENCE: 9369-147
13 <140> CURRENT APPLICATION NUMBER: US/09/645,593
14 <141> CURRENT FILING DATE: 2000-08-25
16 <150> PRIOR APPLICATION NUMBER: 60/151044
17 <151> PRIOR FILING DATE: 1999-08-27
19 <150> PRIOR APPLICATION NUMBER: 60/161,722
20 <151> PRIOR FILING DATE: 1999-10-27
22 <160> NUMBER OF SEQ ID NOS: 25
24 <170> SOFTWARE: PatentIn Ver. 2.0
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 4305
28 <212> TYPE: DNA
29 <213> ORGANISM: Linum usitatissimum
31 <400> SEQUENCE: 1
32 ttcaaaaccc gattcccgag gcggccctat tgaagatatg ggggaagttc gacgagatcg 60
33 atgtcgggtc gagtgctatg gtgatggtgc cgtttggggg gaggatgagc gagatagcca 120
34 agactagcat tccgttccca cacagagttg ggaatttgta ccaaatccaa cacttgtcgt 180
35 attggagcga cgatagggac gcggaaaaac acatccgttg gatcagggag ttgtacgatg 240
36 atctcgagcc ttatgtgtcg aagaatccga ggtatgctta cgtgaactac agggatctcg 300
37 acatcgggat gaatggagga ggtgaagggg atgagaaggg tacttatggt gaggctaagg 360
38 tgtgggggga gaagtacttt ggggtcaact ttgatcggtt ggttcgggtg aagacgattg 420
39 ttgatcccaa taatgtgttt cgaaacgagc agagcattcc ctcaattcca actcggttat 480
40 aaggatcaat gatcaatgag aattttcctt tccaatgtga ttacaagttc tattgggtca 540
41 gctttctcaa ctgctcctat tcatttagat taattcataa caactattaa tttaccagcc 600
42 ttttatccgg cccgttggcc gatttatttt cttaagtttt agatgaaatg aaaccgattt 660
43 agtttttatt gagatgagat taatcttaat ttgcttgaaa tttactcacg gttgatgtga 720
44 tatttggaat taactaaaat gataaatatc ggataaaaat aaaaatattt aaaataaata 780
45 acataaacat aagaacaata aaataaataa atttaatttt aatttatttc cttgttttct 840
46 ttctgtatca tacatctctt ctcttacttc ttaaaggctt ttcaattatc acttaattaa 900
47 atacaataga taaatcgtta attctataac attaacctat acacttgcac ggtgaacaat 960
48 caatatgata atataataat aatataataa ttcaattatt aatctacaat ttttaattaa 1020
49 taaagtttat gcggtcagtt tctgcaagct ccgagctcct tgtcatcgtt agtttctgcg 1080
50 gtctcaaggt ataacgactc ggagcgacga gccctttgct tccaatggac gggttgcatt 1140
51 tctgccgtcg ttgagctcga ttggcgtgtc atgctggagt cagagttcct acaaaaaaac 1200
52 cctaaactag agggtgatta gggtgaaatt agggtgttgg cctgggttcc attgtccaaa 1260
53 gttttagtca acttaaaaac agacttaaat tttatgcttc aaaatagttt atctgttatt 1320
54 atattagcgt gtaattagtc ttgacaatgg ggccggacgg gtacggattc gggaccccga 1380
55 tccccgccca tagtgtaatg gctcaactgc caagtcagca ttggaccgaa attattggac 1440
56 acgaagtact aatgtgaaaa actttacatt tgttattttc tactttaata ctatgctatt 1500
57 ttcaaaattt gaactttaat actatgtttt tatatagttt agtatatctt aatttttatg 1560
58 caaattcatc taattgtatt aaactatttt cgatccgtag ctaattattt cgaaggcaag 1620
59 tcaaagtgtt attgtggact atgtgagcta atattgaacc tttatctctc ccaaccactc 1680
```

```
 60 aagttaattg aaccaaactc gatcggttgg gtttcgagct atttcgagcc attgttgtta 1740
 61 tatgcacgtg agatatcaag attgacccga acactttatt atgataatgt agaaaaagaa 1800
 62 aacatattct aagactacat gcatgcaaag tgcaacccct gcatggaaag ctgctcaaca 1860
 63 cgtggcatag actcccgcca cgtgtccatt ccacctcatc acctcacccc caccgttcac 1920
 64 ctcttattat atcacaacaa tcaatcaatc ctactcctcc atactcgaac aaatccgacc 1980
 65 aacttatacc aatattccca aacttgatta atttctcagc aatatggatc agacgcacca 2040
 66 gacatacgcc ggaaccacgc agaacccgag ctatggcggc gggggcacaa tgtaccagca 2100
 67 gcagcagccg aggtcttacc aggcggtgaa ggcggccact gcagccaccg cgggtggatc 2160
 68 cctcatcgtt ctgtccggtc tcatccttac ggccaccgtc atttcactca tcatagccac 2220
 69 ccctctcctt gtcatcttca gccctgttct tgtcccggct ctcatcaccg tcgggctctt 2280
 70 gatcaccggg tttcttgctt ccggtgggtt cggagtcgcc gccgtcaccg tcttgtcctg 2340
 71 gatctatagg tatgtataag ctttggactt tagtattgtt ataaaataca taagctgatt 2400
 72 tatgaacatg gatctcccaa caagagttat ttaaatgcat tctcggtctg actcgatcgg 2460
 73 ttgggttttg agctactcgg tcacaatggt cgggtcggct ctggatctgt tatactaata 2520
 74 tttggaagcc tgaagtttca ttgttctgcc ccaacttccc actacctttt gagggtgtta 2580
 75 agaagccata caaactaatt atgaatccct cccaacaact cagaactcga gtcagtgggt 2640
 76 tgtgacggtt ctctataaac atttcgaaaa tctttgttca atgaacgtag aaatgaccat 2700
 77 gcttgatgat tgtgggtctt ataaggtacg tgaccggcgg gcacccggcg ggaggggatt 2760
 78 cgctggacca ggctaggtcg aagctggccg gaaaggccag ggaggtgaag gacagggcgt 2820
 79 cggagttcgc acagcagcat gtcacaggtg gtcaacagac ctcttaaaga gagtcctcta 2880
 80 gttaaattgg tcttcgtttc tgtttcgtgg cggcttgtaa actctctttt aagtgtgctg 2940
 81 ttttccttt gtctcgtgtg ttgtaagtga aagtgtaatc gaagttccaa gttggagatg 3000
 82 tttgtaacga tgatgttttc taataatcag agatattaaa agggttgcta atttagtatt 3060
 83 gcgtctgatc tcggaccaaa ctcgcaagta aaattgcaga ggatgagttg tacagaacaa 3120
 84 gcgtgcattg ttctggaagt tcatctcctt ggagccgacc ttgttgcttg cagtttcgcc 3180
 85 aagtccacta gacaatgtta cgagttaagc ctctgtcaaa cagatcgctc tagcgtccca 3240
 86 gaaaacacca gatttttcga aaaccatcgg ggatcaattt tcgattcaat tccgatcttg 3300
 87 gaagtacttg aacagaagca tgatgctaaa agataataga aaatcgaagc ctagaaaagt 3360
 88 tgtacagaaa gcaacaagtc aaaaatatag atcaacttca aaggttcaaa ttacatctta 3420
 89 cagaccccaa aaaatgacag ttaacagaag tcgactaaac agaaaccagc cagcttcacc 3480
 90 tggaatgaag gagctttgat caatccatcc tagcttcatt ccccttgaa attgcagaca 3540
 91 gagctctcat cctgctaaag ctggtggctt attcttaacc ctgcaatcaa taagcatgaa 3600
 92 ctaacattgg acaccttcat cggcggattg ctcgaaaatc agtgagcgag ggatttacct 3660
 93 gtgtgtgtag taacctctct ccttgtacat aaaatctgga aattccggca tcaactactg 3720
 94 ccacctttct gcttaaggtg attttatcac caaggctgag cgtgattcct tgcgtcttgc 3780
 95 tccgaatcct gatgtatcca ctgagctttc catctccttc cttctccagg cttatgttca 3840
 96 ccaatgcgtc ctcgccgaac acactcttgg cgtacaagtt cgcagccagg aatccacact 3900
 97 ctccatcaag tgcagacctg caaaccccaa ataagaacac aaactccaaa gtcaacgatc 3960
 98 aattctccgc cttttatgaa gaaaaggaaa cttctgggta cttacggtgc cgtcagacac 4020
 99 ttcatatttg tagacttgat gatatggtcc aggaattcct tctcgttctg aattgttgtg 4080
100 ttaacagcaa cctgacagac agaaagatat cgcaaattta agatactggg atgactaggc 4140
101 acagagaaat gaaatctaat tctagaagta aaaccttatt ttcccattca aattctgccc 4200
102 acatagtccg gaacgcagca tccgagcaag aagcaggaga gatgtaatcc atgatatcga 4260
103 tgtggatatc gttgaggacg acaactgaac gttccatcac attgg         4305
105 <210> SEQ ID NO: 2
106 <211> LENGTH: 109
107 <212> TYPE: PRT
108 <213> ORGANISM: Linum usitatissimum
110 <400> SEQUENCE: 2
```

```
111 Met Asp Gln Thr His Gln Thr Tyr Ala Gly Thr Thr Gln Asn Pro Ser
112  1               5                  10                  15
114 Tyr Gly Gly Gly Gly Thr Met Tyr Gln Gln Gln Pro Arg Ser Tyr
115             20                  25                  30
117 Gln Ala Val Lys Ala Ala Thr Ala Ala Thr Ala Gly Gly Ser Leu Ile
118         35                  40                  45
120 Val Leu Ser Gly Leu Ile Leu Thr Ala Thr Val Ile Ser Leu Ile Ile
121     50                  55                  60
123 Ala Thr Pro Leu Leu Val Ile Phe Ser Pro Val Leu Val Pro Ala Leu
124 65                  70                  75                  80
126 Ile Thr Val Gly Leu Leu Ile Thr Gly Phe Leu Ala Ser Gly Gly Phe
127                 85                  90                  95
129 Gly Val Ala Ala Val Thr Val Leu Ser Trp Ile Tyr Arg
130             100                 105
133 <210> SEQ ID NO: 3
134 <211> LENGTH: 46
135 <212> TYPE: PRT
136 <213> ORGANISM: Linum usitatissimum
138 <400> SEQUENCE: 3
139 Tyr Val Thr Gly Gly His Pro Ala Gly Gly Asp Ser Leu Asp Gln Ala
140  1               5                  10                  15
142 Arg Ser Lys Leu Ala Gly Lys Ala Arg Glu Val Lys Asp Arg Ala Ser
143             20                  25                  30
145 Glu Phe Ala Gln Gln His Val Thr Gly Gly Gln Gln Thr Ser
146         35                  40                  45
149 <210> SEQ ID NO: 4
150 <211> LENGTH: 3501
151 <212> TYPE: DNA
152 <213> ORGANISM: Linum usitatissimum
154 <400> SEQUENCE: 4
155 tctagacatt tgacataaac cgaattcaaa gaacacaaca ttgactaaca ccaaaaagaa 60
156 atagagtagt gaaatttgga agattaaaaa atagaaacaa actgattctt agaaagaaga 120
157 gatgattagg tgctttcagt tcggtctgtc aggaaatcga gatgttcact tatttacatt 180
158 gtcgattcat ctcccaattg tcctggttcc tttactgtcc gacgcttttt tgaatcccag 240
159 ttaattccca tcaagtcttc cttcagctgc gtagcactgc tagctccaac atggagcgtg 300
160 gagtctactc gttcatgggg catcgcaaag gtttgccttc atgttctgct accagccagc 360
161 gcccaccgcc tcttggttgt gtggacaatt gcggtgaagc gcgcaagttg acatcccata 420
162 gtctcgacac ttcaccatat ggatgtttaa aacgtatatc acgagtgcga tctacatgtc 480
163 ccatcacacc acatataaag caatagtttg ggagcttttc atatttgaaa cgggcattga 540
164 cgacttgccc tctcgataat ttaatctttt tttctcttca gctgattgtg tgcatccatt 600
165 cgggctcaga agcacatcaa agggatctct ccatcgtagt attgggtcgt gtcgtatgat 660
166 acgaagcagt cgatgaagtt tcctaatgtg cgagctacag gctccgcaaa gaacccgcga 720
167 ggtagatcgt atgctagtac ccaaaaatca gtttgtcgta gcggaatcaa cactagagac 780
168 tcaccctaat gcatctcatg tgtgatgaac agtttatcat ttgtgagtct aggggtcatt 840
169 gtcgatgacc caatgcacat tgagcttatg atagaatttg aataggaagc gttttccacc 900
170 cagatcacga atagctaccc cttttttcggg cgccaaattt ccggcatcct atcttccacc 960
171 acaacttaaa gatgcgatcg gtaaggaact caccgaccac acacatcgaa taatcttcgg 1020
172 tgaccggttc ctgttgatca agtccctcaa tttcctcaac ctagtcttca atcgccgcta 1080
173 gcgttatccc ccgcatatgg actttcatag cgcggagcgt agccggagac gacgagcaag 1140
```

```
174 aaggatgagc ggcggcagat tgcggctaaa gaaacgagct tcctgccttg ctctatggag 1200
175 gcagatttct gagttgatgg tgatggattt gtgatgtgga cacttttaat ttaagttgat 1260
176 ttttagcac ttcattcacg taattaaata aataatttcc agtatttat atttatttcc 1320
177 ttacgttatc taattttttg aaagattaaa actttgatat aggcaagatc atgacacgtc 1380
178 gaagttaagt gaatgagact cctaacaagg taataacaaa gcagttcata aaccgaatga 1440
179 ccttgatctt tactaagctt gagatcattg aacatataat taaatacgtt aatgaaagat 1500
180 aagaacttta atataaaaat cattcaaaac gagaaactga taacaaaaac aaagcaaacg 1560
181 gccaacaaaa taatagacgg tggaaggatg atgcagagcc atccaccctt ttttcccagt 1620
182 ttccttactg cttacttctc tatgcatatc acaagacgcc cttgaaactt gttagtcatg 1680
183 cagagccctt actcgccagg tcaccgcacc acgtgttact ctatcacttc tcctcccttt 1740
184 cctttaaaga accaccacgc cacctccctc tcacaaacac tcataaaaaa accacctctt 1800
185 gcatttctcc caagttcaaa ttagttcaca gctaagcaag aactcaacaa caatggcgga 1860
186 tcgtacaaca cagccacacc aagtccaggt ccacacccag caccactatc ccaccggcgg 1920
187 ggctttcggc cgttatgaag gtggactcaa aggcggtcca catcaccagc aaggatcagg 1980
188 cagcggccca tcagcttcca aggtgttagc agtcatgacc gcgctcccca tcggcgggac 2040
189 cctccttgcc ttggccggga taaccttggc tgggacgatg atcgggctgg cgatcaccac 2100
190 cccgattttt gtcatctgca gccctgttct agtcccggcc gctctgctca tcgggtttgc 2160
191 cgtgagcgcg tttctggcct cggggatggc cgggctgaca gggctgacct cgctgtcgtg 2220
192 gtttgcgagg tatctgcagc aggctgggca gggagttgga gtggggtgc cggatagttt 2280
193 cgagcaggcg aagaggcgca tgcaggatgc tgctgggtat atggggcaga agaccaagga 2340
194 agttgggcag gagatccaga ggaagtctca ggatgtgaaa gcatcagaca aataaggtga 2400
195 taataagggg ttttgggttc gtgtgtaaac tggtaaaatg gaaattctgg gttttactgt 2460
196 acttttgcat gtagtggaat gaatgagttc ttgttctctt ttgtcttta atcataaagt 2520
197 aagaagcagc atttcatgtt ctggttgaat attgtcaaga attcgcaaca aatttagcta 2580
198 aaccagttca atcttaccgg ttagacgact tcccagtaag aaacattcca ggtccatccc 2640
199 ggtataagag tctggacttc tgaaaccttt agaccttgga tttggaaaaa agatgaaacc 2700
200 tttagaataa attacaacga tggcagattg tacaaaactg gagtcgagat catgtaaatt 2760
201 agcccataac taagaaccgg cgatgacaac aattactagg aatatggttg ttgggctggt 2820
202 cggcggctag cggtgatgat ttggaagaat cggggatcca gaatgtgaga accgaatcat 2880
203 cgacgaacat tacccggcga ggagcccatt tcaagcaact ttggaactcc tatatggctg 2940
204 ttccagcagg ccacctgctc aagaaagaaa gaagccatgt cagaaatcct tacgaaatct 3000
205 aactggatgc tgatatgaat ccgccaggtg tgcggagttc tttacaggca ggatctataa 3060
206 agaagaaaca tgttttgtat tggcattgtt gatgttccaa gcacgcagcg atctatctcc 3120
207 ggatcctaac aacaaaaata cggattctgt aagaaacaag cgcagaaaac ttctgcaacg 3180
208 aaaccactcg tatatttggt tctgagttgg agaaagatga ccatactact gtatttggtt 3240
209 gaacttggat tggaaccgaa attttgagtt gaaaagcgag tgatcgtata taaatttcag 3300
210 attcagatta ggatatccta tgagagaagg tagagttacc tgatactaca tactgcccat 3360
211 cagggtaaa agttgcctcg atggttgtgt ttggagatgg ttccaggcta aatccacaac 3420
212 gctgaacaaa ttaaaagatg aatggatcaa tcttcaaccc ttacttctgc atttatgagg 3480
213 attggctcaa ggctctctag a                                         3501
```

```
215 <210> SEQ ID NO: 5
216 <211> LENGTH: 180
217 <212> TYPE: PRT
218 <213> ORGANISM: Linum usitatissimum
220 <400> SEQUENCE: 5
221 Met Ala Asp Arg Thr Thr Gln Pro His Gln Val Gln Val His Thr Gln
222   1               5                  10                  15
224 His His Tyr Pro Thr Gly Gly Ala Phe Gly Arg Tyr Glu Gly Gly Leu
225              20                  25                  30
```

```
227 Lys Gly Gly Pro His His Gln Gln Gly Ser Gly Ser Gly Pro Ser Ala
228         35              40               45
230 Ser Lys Val Leu Ala Val Met Thr Ala Leu Pro Ile Gly Gly Thr Leu
231     50              55               60
233 Leu Ala Leu Ala Gly Ile Thr Leu Ala Gly Thr Met Ile Gly Leu Ala
234  65              70               75               80
236 Ile Thr Thr Pro Ile Phe Val Ile Cys Ser Pro Val Leu Val Pro Ala
237             85               90               95
239 Ala Leu Leu Ile Gly Phe Ala Val Ser Ala Phe Leu Ala Ser Gly Met
240         100              105              110
242 Ala Gly Leu Thr Gly Leu Thr Ser Leu Ser Trp Phe Ala Arg Tyr Leu
243     115              120              125
245 Gln Gln Ala Gly Gln Gly Val Gly Val Gly Val Pro Asp Ser Phe Glu
246     130              135              140
248 Gln Ala Lys Arg Arg Met Gln Asp Ala Ala Gly Tyr Met Gly Gln Lys
249 145             150              155              160
251 Thr Lys Glu Val Gly Gln Glu Ile Gln Arg Lys Ser Gln Asp Val Lys
252         165              170              175
254 Ala Ser Asp Lys
255         180
258 <210> SEQ ID NO: 6
259 <211> LENGTH: 1676
260 <212> TYPE: DNA
261 <213> ORGANISM: Linum usitatissimum
263 <400> SEQUENCE: 6
264 tccactatgt aggtcatatc catcatttta attttggggc accattcaat tccatcttgc 60
265 ctttagggat gtgaatatga acggccaagg taagagaata aaaataatcc aaattaaagc 120
266 aagagaggcc aagtaagata atccaaatgt acacttgtca tcgccgaaat tagtaaaata 180
267 cgcggcatat tgtattccca cacattatta aaataccgta tatgtattgg ctgcatttgc 240
268 atgaataata ctacgtgtaa gcccaaaaga acccacgtgt agcccatgca aagttaacac 300
269 tcacgacccc attcctcagt ctccactata taaacccaat atccccaatc ttaccaaacc 360
270 caccacacga ctcacaactc gactctcaca ccttaaagaa ccaatcacca ccaaaaaatg 420
271 gcaaagctga tgagcctagc agccgtagca acgcagttcc tcttcctgat cgtggtggac 480
272 gcatccgtcc gaaccacagt gattatcgac gaggagacca accaaggccg cggtggaggc 540
273 aaggtggcag ggacagcagc agtctgcgag cagcagatcc agcagcgaga cttcctgagg 600
274 agctgccagc agttcatgtg ggagaaagtc cagaggggcg gccacagcca ctattacaac 660
275 cagggccgtg gaggaggcga acagagccag tacttcgaac agctgtttgt gacgacctta 720
276 agcaattgcg caccgcggtg caccatgcca ggggacttga agcgtgccat cggccaaatg 780
277 aggcaggaaa tccagcagca gggacagcag cagggacagc agcaggaagt tcagaggtgg 840
278 atccagcaag ctaaacaaat cgctaaggac ctccccggac agtgccgcac ccagcctagc 900
279 caatgccagt tccagggcca gcagcaatct gcatggtttt gaaggggtga tcgattatga 960
280 gatcgtacaa agacactgct aggtgttaag gatggataat aataataata atgagatgaa 1020
281 tgtgttttaa gttagtgtaa cagctgtaat aaagagagag agagagagag agagagagag 1080
282 agagagagag agagagagag agaggctgat gaaatgttat gtatgtttct tggtttttaa 1140
283 aataaatgaa agcacatgct cgtgtggttc tatcgaatta ttcggcggtt cctgtgggaa 1200
284 aaagtccaga agggcggccg cagctactac tacaaccaag gccgtggagg agggcaacag 1260
285 agccagcact tcgatagctg ctgcgatgat cttaagcaat tgaggagcga gtgcacatgc 1320
286 aggggactgg agcgtgcaat cggccagatg aggcaggaca tccagcagca gggacagcag 1380
287 caggaagttg agaggtggtc ccatcaatct aaacaagtcg ctagggacct tccgggacag 1440
```

<210> 8
<211> 4999
<212> DNA
<213> Linum usitatissimum

<400> 8

```
ctcaagcata cggacaaggg taaataacat agtcaccaga acataataaa caaaaagtgc 60
agaagcaaga taaaaaaatt agctatggac attcaggttc atattggaaa catcattatc 120
ctagtcttgt gaccatcctt cctcctgctc tagttgagag gccttgggac taacgagagg 180
tcagttggga tagcagatcc ttatcctgga ctagcctttc tggtgtttca gagtcttcgt 240
gccgccgtct acatctatct ccattaggtc tgaagatgac tcttcacacc aacgacgttt 300
aaggtctcta tcctactcct agcttgcaat acctggcttg caatacctgg agcatcgtgc 360
acgatgattg gatactgtgg aggaggagtg tttgctgatt tagagctccc ggttgggtga 420
tttgacttcg atttcagttt aggcttgttg aaatttttca ggttccattg tgaagccttt 480
agagcttgag cttccttcca tgttaatgcc ttgatcgaat tctcctagag aaaagggaag 540
tcgatctctg agtattgaaa tcgaagtgca catttttttt caacgtgtcc aatcaatcca 600
caaacaaagc agaagacagg taatctttca tacttatact gacaagtaat agtcttaccg 660
tcatgcataa taacgtctcg ttccttcaag aggggttttc cgacatccat aacgacccga 720
agcctcatga aagcattagg gaagaacttt tggttcttct tgtcatggcc tttataggtg 780
tcagccgagc tcgccaattc ccgtccgact ggctccgcaa aatattcgaa cggcaagtta 840
tggacttgca accataactc cacggtattg agcaggacct attgtgaaga ctcatctcat 900
ggagcttcag aatgtggttg tcagcaaacc aatgaccgaa atccatcaca tgacggacgt 960
ccagtgggtg agcgaaacga aacaggaagc gcctatcttt cagagtcgtg agctccacac 1020
cggattccgg caactacgtg ttgggcaggc ttcgccgtat tagagatatg ttgaggcaag 1080
acccatctgt gccactcgta caattacgag agttgttttt tttgtgattt tcctaagttt 1140
ctcgttgatg gtgagctcat attctacatc gtatggtctc tcaacgtcgt ttcctgtcat 1200
ctgatatccc gtcatttgca tccacgtgcg ccgcctcccg tgccaagtcc ctaggtgtca 1260
tgcacgccaa attggtggtg gtgcgggctg ccctgtgctt cttaccgatg ggtggaggtt 1320
gagtttgggg gtctccgcgg cgatggtagt gggttgacgg tttggtgtgg gttgacggca 1380
ttgatcaatt tacttcttgc ttcaaattct ttggcagaaa acaattcatt agattagaac 1440
tggaaaccag agtgatgaga cggattaagt cagattccaa cagagttaca tctcttaaga 1500
aataatgtaa cccctttaga ctttatatat ttgcaattaa aaaaataatt taactttag 1560
actttatata tagtttttaat aactaagttt aaccactcta ttatttatat cgaaactatt 1620
tgtatgtctc ccctctaaat aaacttggta ttgtgtttac agaacctata atcaaataat 1680
caatactcaa ctgaagtttg tgcagttaat tgaagggatt aacggccaaa atgcactagt 1740
attatcaacc gaatagattc acactagatg gccatttcca tcaatatcat cgccgttctt 1800
cttctgtcca catatcccct ctgaaacttg agagacacct gcacttcatt gtccttatta 1860
cgtgttacaa aatgaaaccc atgcatccat gcaaactgaa gaatggcgca agaacccttc 1920
ccctccattt cttatgtggc gaccatccat ttcaccatct cccgctataa aacacccca 1980
tcacttcacc tagaacatca tcactacttg cttatccatc caaaagatac ccaccatggc 2040
tagatcatca agccctttgc ttctctcact ctgcattttc gccattctct tccactcttc 2100
tctgggtagg cagcaattcc agcaggggaa cgagtgccag atcgacagga tcgacgcatc 2160
cgagccggac aaaaccatcc aggcagaagc tggcaccatc gaggtatggg accagaaccg 2220
ccagcaattc cagtgcgctg gtgttgccgt tgtaaggcgc accattgagc ccaaaggtct 2280
tctcttgcct ttctacagca acacccctca gctcatctac atcgttcaag gtataaatta 2340
aatcagttca tacaatgata accaccactt cgaatgtatt tatcaaatat caatgatcga 2400
tgcacctgta tgtgttgtgt atattcaggt aggggagtta caggaatcat gttcccakga 2460
tgtccagaga cattcgagga atcccagcag caaggacaac agggccaaca gggtagttcc 2520
caagaccagc accagaagat ccgccgcttc cgtgaaggtg acgtcattgc cgtccctgcc 2580
ggtgtagccc actggtccta caacgatggc aacgaaccag tcatggccat tgttgtccat 2640
gacacttcca gccacctcaa ccaactggac aacaacccca gggtatataa gcattgccgt 2700
agttgctaat aaaattgcaca caattggaac tctattttca gtatctaata acttttttcct 2760
tttttggcag aacttctact tggcaggaaa cccgagagac gagttcgaac aatcgcagca 2820
aggaggcagg ctgagccgtg gggagagtga aggtggacga ggacgcaggg aacctcttca 2880
acctgcaaca acctcttctt gcggaatcga ctccaagctc atcgcggagg cgttcaatgt 2940
cgacgagaac gtggcaagga ggctacagag cgagaacgac aacagaggcc agatcgtccg 3000
agtcgaaggc gagctcgaca tcgtcagacc tccgaccagt atccaggagg agtcacagga 3060
```

```
gcagggaggt cgtggtggtg gccgctacta ctccaatgga gtggaggaga ccttctgctc 3120
catgagacta attgagaaca tcggcgatcc ttctcgggca gacattttca ctccagaagc 3180
cggccgcgtt agatccctca acagccacaa cctccccgtc ctgcaatgga tccagcttag 3240
cgccgagaga ggcgttctct acaatgtata gatctcactc acgcaccaac tctaaattga 3300
atccctaatt atttaattca ccgatatctg accgaccggt ttgaattttg taggaagcga 3360
tcaggctgcc gcactggaac atcaacgcac acagcatagt gtacgcgatc agaggacaag 3420
ccagagtcca gatcgtgaac gaggaaggga attcggtgtt cgatggagtg ctgcaggaag 3480
gacaggtggt gacggtgccg cagaacttcg cggtggtaaa gagatccag agcgagaggt 3540
ttgagtgggt ggcgttcaag accaacgaca acgcgatggt gaactcgcta gccgggagga 3600
catcggcagt aagggcgatc cccgcggatg tactggctaa cgcctggagg gtgtcgccgg 3660
aggaggcgag gagggtgaag ttcaacaggc aggagactca cttggctagc accaggggcc 3720
agtccaggtc gcccgggagg ttgaatgtcg tcaaggaggt gatcaacttg cttatgtaaa 3780
atgtgacggt gaaataataa cggtaaaata tatgtaataa taataataat aaagccacaa 3840
agtgagaatg aggggaaggg gaaatgtgta atgagccagt agccggtggt gctaattttg 3900
tatcgtattg tcaataaatc atgaattttg tggttttat gtgtttttt aaatcatgaa 3960
ttttaaattt tataaaataa tctccaatcg gaagaacaac attccatatc catggatgtt 4020
tctttaccca aatctagttc ttgagaggat gaagcatcac cgaacagttc tgcaactatc 4080
cctcaaaagc tttaaaatga acaacaagga acagagcaac gttccaaaga tcccaaacga 4140
aacatattat ctatactaat actatattat taattactac tgcccggaat cacaatccct 4200
gaatgattcc tattaactac aagccttgtt ggcggcggag aagtgatcgg cgcggcgaga 4260
agcagcggac tcggagacga ggccttggat gagcagagtc tttacctgcc agggcgtgaa 4320
ggggaagagc ggccttctgg agtaggagtt cagcaagcgg cggttccttg gcggagtaag 4380
cggacgtaag ggtgantgtc gacgtantcg tttcnggagg cgnattcatg aagggttaaa 4440
gtcanatctg tagctctcga gtgctcaggg agccnaaaga cgntgggaaa ccgtcgncgt 4500
ttgggcatc agtcngcggg gcacgcttcc ctcctgctgc tccanaancn angtanattt 4560
aaaaganatg ggaaattaan taatggnaat nannaggagg attgnaacgg tcnganccgn 4620
angaanagtt tttannggtt taaatactgg gggagtngna gccngccnct ggttccngtg 4680
tagangaaac caagnnccgg gaggnttnca nnngnnaggg agaaaaagga nncatttnan 4740
nangcngagg gacatgaanc ggtacngagc tgnggttcan nnancggcgn nnggnagtcc 4800
cnngggaccn ggntgggtn anaagggaan ggaacattng gtngnangga naanacntt 4860
ttacnattgc ctttgcaggn nngtntnggc ncntncgggt nacatnccgc tgcatgggct 4920
ttgggggngcc nanaggnagc cncanggna nncngccncc ttgtncangn cgctnaagtt 4980
cnattgtana tggncgttg                                        4999
```

Please explain all n's in the sequence. The circled n's are a sample.

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Input Set : A:\Sequence
Output Set: N:\CRF3\09072000\I645593.raw

L:13 M:270 C: Current Application Number differs, Replaced Application Number
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:412 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:412 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:412 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:412 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:412 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8
L:413 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:413 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:413 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:413 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
M:340 Repeated in SeqNo=8
L:414 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:414 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:414 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:414 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:415 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:415 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:415 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:415 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:416 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:416 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:416 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:416 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:417 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:417 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:417 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:417 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:418 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:418 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:418 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:418 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:419 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:419 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:419 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:419 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:420 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:420 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:420 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:420 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:421 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:421 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:421 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:421 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:422 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:422 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:422 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:422 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8

```
L:455 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:10
L:455 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10
L:455 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:455 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10
L:455 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10
```